

Supplemental Table 1

Locus/ unit	CpG site ¹	Location, success rate and SNPs	Regulatory function	² SGA-AGA, P-value
<i>IGF2</i> DMR³		chr11:2126035-2126372	DMR, ass. with bi-allelic <i>IGF2</i> expression, imprinted	
<i>IGF2</i> _01	Unit 1	Excluded for rs3741208 and rs17883577		
<i>IGF2</i> _02	Unit 2	Excluded for rs3741209		
<i>IGF2</i> _03	CpG_5	100%		1.5%, 0.66
<i>IGF2</i> _04	CpG_4	99.1%		-2.3%, 0.93
<i>IGF2</i> _05	Unit 5	Excluded for rs4930041		
<i>IGF2</i> _06	CpG_2&3	100%	PAX-6 binding site	0.1%, 0.15
<i>IGF2</i> _07	CpG_1	98.2%		-0.3%, 0.14
<i>GNASAS</i>		chr20:56859210-56859503	DMR, promoter region of the antisense transcript influencing GNAS expression, imprinted	
<i>GNASAS</i> _01	CpG_1&2	94.7%		-0.5%, 0.59
<i>GNASAS</i> _02	CpG_3&4	96.5%		-0.6%, 0.49
<i>GNASAS</i> _03	CpG_5	84.1%		-2.1%, 0.16
<i>GNASAS</i> _04	CpG_6	96.5%		-0.4%, 0.63
<i>GNASAS</i> _05	CpG_7	97.3%		-0.6%, 0.46
<i>GNASAS</i> _06	CpG_8&9	97.3%	Transfac putative TFBS	-0.4%, 0.59
<i>GNASAS</i> _07	CpG_10-12	96.5%	Transfac putative TFBS	-0.2%, 0.82
<i>GNASAS</i> _08	CpG_13&14	98.2%	Transfac putative TFBS	-0.6%, 0.48
<i>GNASAS</i> _09	CpG_15	95.6%		-0.4%, 0.65
<i>GNASAS</i> _10	CpG_16	Excluded for rs45596642		-0.6%, 0.47
<i>GNASAS</i> _11	CpG_17-19	96.5%	P300 binding site	0.0%, 1.00
<i>INSIGF</i>		chr11:2138912-2139216	DMR, Promoter region of INS and INSIGF, imprinted	
<i>INSIGF</i> _01	CpG_1	Low mass		
<i>INSIGF</i> _02	CpG_2	99.1%, 10124 failed → AGA??		-0.1%, 0.89
<i>INSIGF</i> _03	CpG_3	99.1%	Transfac putative TFBS	-0.4%, 0.76
<i>INSIGF</i> _04	CpG_4	99.1%		-0.2%, 0.86

<i>INSIGF</i> 05	CpG 5	99.1%	Transfac putative TFBS	-0.1%, 0.82
<i>INSIGF</i> 06	CpG 6	99.1%		-0.1%, 0.76
LEP		chr7:127668290-127668646	Promoter region, methylation influences transcription, not imprinted	
<i>LEP</i> 01	CpG 1	98.2%		-0.4%,0.72
<i>LEP</i> 02	CpG 2-7	High Mass and rs791620		
<i>LEP</i> 03	CpG 8	100%		0.0%, 0.95
<i>LEP</i> 04	CpG 9&10	Mass overlap with unit 9		
<i>LEP</i> 05	CpG 11	Mass overlap with units 12 and 6		
<i>LEP</i> 06	CpG 12&13	Mass overlap with units 5 and 12		
<i>LEP</i> 07	CpG 14&15	Mass overlap with unit 14		
<i>LEP</i> 08	CpG 16&17	99.1%		-0.7%, 0.30
<i>LEP</i> 09	CpG 18	Mass overlap with unit 4		
<i>LEP</i> 10	CpG 19-21	100%		-0.9%, 0.23
<i>LEP</i> 11	CpG 22	95.6%	C/EBPbeta,c-Myb, MIF-1	-3.7%, 0.12
<i>LEP</i> 12	CpG 23&24	Mass overlap with units 5 and 6		
<i>LEP</i> 13	CpG 25	94.7%	Sp1 binding site, methylation important for transcription	-1.8%, 0.42
<i>LEP</i> 14	CpG 26	Mass overlap with unit 7		
<i>LEP</i> 15	CpG 27	Low mass		
<i>LEP</i> 16	CpG 28	46.7%, low success due to partial overlap		
<i>LEP</i> 17	CpG 29	Excluded for rs2167270		
<i>LEP</i> 18	CpG 30-32	High Mass		

1. CpG sites are numbered from the sequence identical to the forward primer sequence. The PCR primers were reported earlier by Tobi *et al.* Hum. Mol. Genet. 2009 and Talens *et al.* FASEB J. 2010. For completeness (without Epityper 10mer and T7 tags): IGF2 DMR Forward: 5'TGGATAGGAGATTGAGGAGAAA Reverse: 5'AAACCCCAACAAAAACCACT. GNASAS Forward: 5'GTAATTTGTGGTATGAGGAAGAGTGA Reverse: 5'TAAATAACCCAACTAAATCCCAACA. INSIGF Forward: 5'GTTTTGAGGAAGAGGTGTTGA Reverse: 5'ACCTAAAATCCAACCACCCTAA. LEP Forward: 5'GTTTTTGGAGGGATATTAAGGATTT Reverse: 5'CTACCAAAAAAACAACAAAAAAA

2. The difference in DNA methylation between the small for gestational age and appropriate for gestational age groups. A negative difference means that the SGA group has a lower methylation level. A two-sided P-value resulting from a linear mixed model corrected for the correlation between individual CpG dinucleotides, bisulfite batch and sex between the SGA and AGA groups.

3. In Heijmans & Tobi et al., PNAS 2008 the sites we reported the CpG sites from the centromere onwards.